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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:39:30; Search time 79 Seconds (without alignments)

86.070 Million cell updates/sec

Title: US-09-989-481-4

Perfect score: 192
Sequence: 1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
```

#

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Listing first 45 summaries

671580

671580 seqs, 206047115 residues

earched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### SUMMARIES

					COTTON	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ΙΟ	Description
ri	56.5	29.4	111	Ŋ	096868	096868 heliocidari
~	56.5	29.4	111	S	698960	096869 heliocidari
m	56.5	29.4	196	16	Q8VJS3	Q8v1s3 mycobacteri
4	56.5	29.4	223	16	Q10843	Q10843 mycobacteri
'n	56.5	29.4		9	Q95MP1	095mpl bos taurus
9	56.5	29.4		7	6NN26O	Q9znn9 comamonas t
. 7	56.5	29.4		~	Q9S150	Q9s150 comamonas t
æ	56.5	29.4		Ŋ	Q8WSN8	
6	55	28.6		æ	Q8SME7	Q8sme7 globba plat
10	55	28.6		10	Q9XFS2	Q9xfs2 arabidopsis
11	54.5	28.4		9	Q9N2C2	Q9n2c2 oryctolagus
12	54	28.1		m	Q90T16	Q9ut16 schizosacch
13	54	28.1		16	Q9AAP0	Q9aap0 caulobacter
14	53.5	27.9		11	Q8R057	Q8r057 mus musculu
15	53.5	27.9		11	Q924K1	Q924k1 mus musculu
16	53.5	27.9		9	Q95MN8	Q95mn8 papio cynoc

095mn7 saimiri bol 09n871 homo saplen 09b873 homo saplen 095mn9 pan paniscu 095mp0 macaca mula 013051 homo saplen 09auv9 oryza sattv 09tb53 corynebacter 09a21 canlobacter 09a21 canlobacter 09455 corynebacter 09a45 pseudomonas 081510 arabidopsis 081510 arabidopsis 081510 arabidopsis 081510 persea indi 099hq8 persea indi 099hq8 persea indi 099hq8 persea indi 099hq5 persea indi 099hq6 persea indi 098x91 servema arc	10007
6 Q95MN7 4 Q9N8310 6 Q95MN9 6 Q95MN9 6 Q95MN9 2 Q9AU9 2 Q9AU9 2 Q9AU3 10 Q9AU3 11 Q9AU3 11 Q9AU3 11 Q9AU3 12 Q9AU3 10 Q9AU3 10 Q9AU3 11 Q9AU3 12 Q9AU3 13 Q9GU3 14 Q9GU3 16 Q9RU3 16 Q9RU3 16 Q9RU3 17 Q9RU3 18 Q9GU3 19 Q9RU3 19 Q9GU3 10 Q9RU3 10 Q9RU3 10 Q9RU3 10 Q9RU3 11 Q9	8 Q8SKU5 8 Q8SKU5 8 Q8SE29 10 Q8VWJ4
7.9 7.9 7.9 7.9 7.9 7.1 7.1 7.1 7.1 7.1 7.1 7.1 7.1	
23.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	51 26 51 26 51 26 51 26
74 74 75 75 75 75 75 75 75 75 75 75	14444 10640

#### ALIGNMENTS

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RESULT 2

126 FAGDSRRANLW---AADRYNRAIARGHDHP 152

096869

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Mycobacterium tuberculosis.
                                                   PRELIMINARY;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                 Q10843
Q10843;
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Q10843
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STRAIN-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dosnon R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermclaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                        MEDLINE-98320638; PubMed-9656482;
Ferkowicz M.J., Stander M.C., Raff R.A.;
"Phylogenetic relationships and developmental expression of three sea
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                    Heliocidaris tuberculata (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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                                                                                                                                                                                                                                                                                                                                   Match 29.4%; Score 56.5; DB 5; Length 111; Local Similarity 50.0%; Pred. No. 1.4; hes 12; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003346; Transposase_20.
Pfam; PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;
                                                                                                                                                                                                                                                                                                111 111
111 AA; 12341 MW; A858F5718F38BD4D CRC64;
                         U1-WAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) cell signaling molecule Wnt-5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
 111 AA
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                                                                                                                                                                                                                      MO1. Biol. Evol. 15:809-819(1998).
EMBL, U58984; AAC69435.1; -.
InterPro; IPR000970; Wnt_grthfactor.
Pfam; PF00110; wnt; 1.
SMART; SM00097; WNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                    11 CWM-LSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                             urchin Wnt genes.";
Mol. Biol. Evol. 15:809-819(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR 2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, IS1607, transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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Best Local Similarity 46.7%
 PRELIMINARY;
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=7635;
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                       01-MAY-1999 (
01-MAY-1999 (
01-JUN-2002 (
                                                                                                                          Heliocidaris.
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SEQUENCE
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Q8VJS3;
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096869;
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FWGDT -- LNCWMLSAFSRYARCLAEGHDGP 31

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CTRAIN-H37RY.

COLESTAIN-H37RY.

COLESTAIN-H37RY.

COLESTAIN-B3295987; PubMed-9634230;

COLESTAIN-H37RY.

COMPLETER R., Dearly R., Falthell T., Connor R., Mollestain R., Skelton R., Skelton S., Squares S., Squares R., Skelton S., Bociphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

Nature 393:537-544(1998).

C. I. SIMILARITY: TO M.PARATUBERCULOSIS IS900.
                                                                                                                                                                                                                                                                                                                                                                 <u>`</u>
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                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae, Bos.
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Sohocki M.M., Sullivan L.S., Tirpak D.L., Daiger S.P.;
"Comparative analysis of aryl-hydrocarbon receptor interacting
protein-like 1 (Alpli), a gene associated with inherited retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculist; Rv2014; -...
InterPro; IPR003346; Transposase_20.
Pfam; Pr02371; Transposase_20; Pfam; Pr02371; Transposase_20; Hypothetical protein; Complete proteome.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (T-EMBLrel. 19, Last sequence update) 01-MAR-2002 (T-EMBLrel. 20, Last annotation update) Aryl-hydrocarbon interacting protein-like 1.
                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.4%; Score 56.5; DB 16; Best Local Similarity 46.7%; Pred. No. 2.8; Matches 14; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 AA.
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01-NOV-1998 (TriMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequely-NOV-1998 (TrEMBLrel. 20, Last annow Hypothetical protein Rv2014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
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EMBL; AF2964.0; ARK77954.1; -.
InterPro; IPR01440; TPR.
Ffam: PF00515; TPR; 2.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024776; AAL32241.1; -
InterPro; IPR000536; Hormone_rec_lig.
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                                                                                                                                                                                                                                                                                                                                                        29.4%; Score 56.5; Di
33.3%; Pred. No. 7.5;
tive 3; Mismatches
                                                                                                                                  EMBL, AB024741; BAA87867.1; -.
InterPro; IPR005199; AAA_ATPase.
InterPro; IPR005197; HTH_F18.
InterPro; IPR005078; Sig54_Interact.
InterPro; IPR004096; V4R.
InterPro; IPR0954; HTH_8; 1.
Pfam; PP00158; Sigma54_activat; 1.
Pfam; PP02830; V4R; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 33.3
nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Geisel C., Lamar B.;
"The sequence of C. el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission.";
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            SEQUENCE FROM N.A.
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Best Local S
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Q8WSN8
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                                                                                                                                                                                                                                           Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
NCBI_TaxID=285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Microbiology 144:2895-2903(1998).
-1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                      STRAIN-TA441;
MEDLINE-99018839; PubMed-9802031;
Arai H., Akahira S., Ohishi T., Maeda M., Kudo T.;
Adaptation of Comamonas testosteroni TA441 to utilize phenol:
organization and regulation of the genes involved in phenol
degradation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.4%; Score 56.5; DB 2; Length 565; 33.3%; Pred. No. 7.2; .ive 3; Mismatches 6; Indels 2
                         Length 328;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0675; SIGMAS4_INTERACT_1; 1.
PROSITE; PSO0676; SIGMAS4_INTERACT_2; UNKNOWN_1.
PROSITE; PSO0688; SIGMAS4_INTERACT_3; 1.
PROSITE; PSO0688; SIGMAS4_INTERACT_4; 1.
ATP-binding; DNA-binding; Transcription regulation.
SEQUENCE 565 AA; 62649 MW; D6D0F0AD984D3201 CRC64;
328 AA; 38472 MW; B2B5E7ACF5E0A72A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Positive regulator of phenol-degradative genes.
                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                11;
                         DB 6;
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                       Query Match 29.4%; Score 56.5; Di
Best Local Similarity 43.3%; Pred. No. 4.1;
Matches 13; Conservative 5; Mismatches
                                                                                    584 AA
                                                                         4 FWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB006480; BAA34177.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR002197; HTH-Fis.
InterPro; IPR002078; S1954_Interact.
InterPro; IPR004096; V4R.
                                                                                                                                                                                     Created)
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Pfam; PF03158; Sigma54_activat; 1.
Pfam; PF02130; V4R; 1.
PRINTS; PR01590; HTHFIS.
SWART; SW03182; AAA; 1.
TIGRFAMS; TIGR01199; HTH_f1s; 1.
                                                                                                                                                             PRT;
                                                                                                                                                                      Q9ZNN9;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
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hes 18; Conservative
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APHR.
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Matches 18
SEQUENCE
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Q9S150;
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STRAIN-R5;
MEDLINE-2005576.; PubMed-10589844;
Teramoto M., Futamata H., Barayama S., Watanabe K.;
Teramoto M., Futamata H., Barayama S., Watanabe K.;
Characterization of a high-affinity phenol hydroxylase from Comamonas testosteroni R5 by gene cloning, and expression in Pseudomonas aeruginosa PAOIC...;
... Canat 262:558(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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NCBI_TaxID=6239;
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                                                                                                                                                                                                            MOI. Gen. Genet. 262:552-558(1999).
-!- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WG--DTLNCWML----SAFSR-----YARCLAEG---HDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid Y41D4B."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PROJECT, TAK, I.

PRINTS, PROJECT, AAA; I.

FIGREAMS, TICROLISS, HTH_fis; I.

PROSITE; PSO0675; SIGMA54_INTERACT_1; I.

PROSITE; PSO06676; SIGMA54_INTERACT_2; UNKNOWN_1.

PROSITE; PSO0686; SIGMA54_INTERACT_3; I.

PROSITE; PSO0686; SIGMA54_INTERACT_4; I.

ATP-binding; DNA-binding; Transcription regulation.

SEQUENCE 584 AA; 64666 MW; 94AB4D5612513158 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 77.4 kDa protein.
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Sequence

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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                  E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
 nucleotide-and calmodulin-regulated ion channels in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. V. features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of rabbit cDNA for lipocalin-type prostaglandin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Y17912; CAB40129.1; -.
EMBL; AR010695; BAB10748.1; -.
EMBL; AX057691; AAL15321.1; -.
InterPro; IPR0000536; NAPP_binding.
InterPro; IPR0000536; M+channel_nig.
Pfam; PF00227; cNMP_binding; 1.
Pfam; PF00227; cNMP_binding; 1.
Pfam; PF00220; comp. in. trans; 1.
SMART; SM00100; cNMP; 1.
PROSITE; PS00102; cNMP; 1.
PROSITE; PS0042; CNMP_BINDING_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 694;
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                                                                                                                   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthase.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus
                                                                                                                                                                          STRAIN-COLUMBIA;
MEDLINE-98344145; PubMed-9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 GTVWWGIALNMIAYFVAAHAAGACWYLLGVQRSAKCLKE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GT-FWGDTLN------CWMLSAFSRYARCLAE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
Prostaglandin D synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 10;
Pred. No. 15;
2; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.6%; Score 55; 35.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P80188; IDFV.
InterPro; PR002345; Lipocalin.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakau H., Fujimori K., Urade Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB040991; BAA94343.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 35.9
Matches 14; Conservative
                                 Plant J. 18:97-104(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scker J.R.;
                         chaliana.
                                                                                                                                                                                                                                  Pabata S
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Q9N2C2;
                                                                                                     Koehler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta, Lilliopsida; Zingiberales, Zingiberaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takano A., Okada H.;
"Multiple occurrences of triploid formation in Globba (Zingiberaceae)
from molecular evidence.";
Plant Syst. Evol. 230:143-159(2002).
EMBL; AB049250; BAB85874.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                            DB 5; Length 680;
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MEDLINE-99272993; PubMed-10341447;
Kohler C., Merkle T., Neuhaus G.;
"Characterisation of a novel gene family of putative cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Length 515;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
               Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR000047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
Hypothetical protein.
SEQUENCE 680 AA; 77412 MW; F870B89A2C162305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 AA; 62022 MW; DE784AD0C3F48B5A CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cyclic nucleotide and calmodulin-regulated ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                          Score 56.5; Di
Pred. No. 8.8;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                            42 WGEPVNCCEIVSTGSAFCKSCRFAKCLAVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 WTDLADCDIINRFSRICRKLSHYHSGSSK 426
                                                                                                                                                                                                                                                                    5 WGDTLNCWML----SAF---SRYARCLAEG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                                       515
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                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
InterPro; IPR001628; Znf_C4steroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%;
ilarity 34.5%;
Conservative
                                                                                                                                                                                            ch 29.4%;
l Similarity 43.3%;
l3; Conservative
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21,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Q8SME7;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Globba platystachya.
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CNGC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=138161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
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Globba.

Q8SME7

RESULT 9 **DBSME7** 

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Matches

Q9XFS2

RESULT 10

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Q9XFS2

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316 AN; 35026 MW; 41C4289216FED963 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Moise).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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         SEQUENCE
                                                                                                                                                                                                                                                                                                                           08R057;
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                                                                                                                                                                                                                                                                                                      Q8R057
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QBR057
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Wedler H., Duesterhoeft A., Lyne M.H., Rajandream M.A., Barrell B.G.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121764; CAB57430.1; -.
SEQUENCE 287 AA; 33149 MW; 21F78CCD7B2FFD97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. US.A. 98:4136-4141(2001).
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                  Length 191;
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                                                                                                                                          Indels
                            UNKNOWN_1.
; 1424BD9878512F61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                          13;
                                                                                           Score 54.5; DB 6;
Pred. No. 4.6;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                   287 AA.
                                                                                                                                                                                                            5 WGDTLNCWMLSA-FSRYARCLAEGHDGPTQ 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast atpl2 protein precursor homolog SPAC9.12C.
                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TIEMBLIEL: 13, Created) 01-MAY-2000 (TIEMBLIEL: 13, Last sequ 01-MAY-2000 (TIEMBLIEL: 13, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; Pubmed-11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 WLSSLNSWOLAAFERSVSC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 WGDTLNCWMLSAFSRYARC 23
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; UI
SEQUENCE 191 AA; 21444 MW;
                                                                                           Query Match
Best Local Similarity 33.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein CC0557.
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                   Q9UT16;
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Q9UT16
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Sohocki M.M., Sullivan L.S., Tirpak D.L., Daiger S.P.;
"Comparative analysis of aryl-hydrocarbon receptor interacting
protein-like 1 (Alpli), a gene associated with inherited retinal
disease in humans."
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          Length 316;
                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TIEMBLIE). 21, Last sequence update)
01-JUN-2002 (TIEMBLIE). 21, Last annotation update)
Similar to aryl-hydrocarbon interacting protein-like 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aryl-hydrocarbon interacting protein-like 1.
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Query Match 28.1%; Score 54; DB:
Best Local Similarity 56.2%; Pred. No. 9.2;
Matches 9; Conservative 2; Mismatches
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44.8%; Pred. No. 6.1;
tive 4; Mismatches
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ilarity 44.8%; Pred. No. 11;
Conservative 4; Mismatches
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EMBL; AF296412; AAK77956.1; -.
                                                                                                                                                                                                                                                                      301 GDILSCWKLGAVPRYS 316
                                                                                                                                                                                                               6 GDTLNCWMLSAFSRYA 21
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR001440; TPR.
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87 FWCDTIHTGVYPMLSRSLRQVAEGKD-PT 114

Search completed: May 29, 2003, 15:45:02 Job time: 82 secs

OM protein - protein search, using sw model

May 29, 2003, 15:34:05; Search time 22 Seconds (without alignments) 62.214 Million cell updates/sec Run on:

US-09-989-481-4 192 1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues earched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ι α	Q9jlg9 rattus norv	Q9nzn9 homo sapien			P24240 escherichia	P01133 homo sapien		_	Q9aev8 burkholderi	O69115 burkholderi	P32666 escherichia	Q9fzw7 bacteriopha		Q9s646 pseudomonas			Q59097 alcaligenes		P41955 caenorhabdi	P31895 rhodospiril	Q37888 bacteriopha	P55037 synechocyst	_	~	P48602 drosophila	Q99p87 mus musculu	N	P49027 oryza sativ		O9pac7 xylella fas		075962 homo sapien
SUMMARIES	ID	IMB2_SCHPO	AIPL_RAT	AIPL_HUMAN	LIP1_GEOCN	CGA1_XENLA	ASCB_ECOLI	EGF_HUMAN	GBA2_NEUCR	ENV_HV1S1	APAH_BURMA	APAH_BURPS	PEPE_ECOLI	HEAD_BPGA1	AGRI_RAT	PPK_PSEAE	POLG_KUNJM	NARB_SYNP7	ODP1_ALCEU	C560_CAEEL	C560_CAEBR	COOH_RHORU	HEAD_BPB03	GLTB_SYNY3	ITB4_HUMAN	YF81_XYLFA	VAA1_DROME	RSN_MOUSE	NEU4_ONCKE	GBLP_ORYSA	VE2_HPV60	PPK_XYLFA	SOL_DROME	TRIO_HUMAN
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æ	Query	30.7		27.9	27.1	9.97	56.6	26.6	25.8	25.8	25.5	25.5	25.0	25.0	25.0	24.5	24.5	24.2	24.2	24.0	24.0	24.0	24.0	24.0	24.0	23.7	23.7	23.4	23.4	23.4	23.4	23.4	23.4	23.4
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	Q08869 pasteurella P80147 sus scrofa P50554 rattus norv				
POLG_WNV PGHD_FELCA	PLPB_PASHA GABT_PIG GABT_RAT	VAA1_BOVIN VAA1_HUMAN	VAA1_MOUSE VAA1_PIG	AMPN_PIG INF_MELGA	CFAD_HUMAN
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3430 191	276 500 500	617 617	617 617	962 192	253
23.4	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	23.2	23.2	7 7 7 7 7 7 7	22.5
45	44 44.5 5.5 5.5	44.5	44.5	44.5 44	44
34 35	36 37 38	39 40	4 1 1 2	<b>44</b>	45

### ALIGNMENTS

RESULT 1  IMB2_SCHPO  AC OIA03  DDT 15-DB  DT 15-DB  CO C Schizr  CO C
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PPIASE, FKBP-TYPE.

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   and for commercial
            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schocki M.M., Bowne S.J., Sullivan L.S., Blackshaw S., Cepko C.L., Payne A.M., Bhattacharya S.S., Khaliq S., Mehdi Q., Birch D.G.; Harrison W.R., Elder F.F.B., Reckenlively J.R., Daiger S.P.; "Mutations in a novel photoreceptor-pineal gene on 17p cause Leber congenital amaurosis."; Nat. Genet. 24:79-83(2000).

-I TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RETINA.
-I SIMILARITY: BELOMGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                       ö
                                                                            PROSITE; PS50166; IMPORTIN_B_NT; FALSE_NEG.
Hypothetical protein; Transport; Protein transport; Repeat.
DOMAIN 34 122 IMPORTIN N-TERMINAL.
                                                                                                                                                                                                                                                Score 59; DB 1; Length 910;
Pred. No. 2;
4; Mismatches 9; Indels
   Usage by
                                                                                                                                                                                                                  185 ASP/GLU-RICH (ACIDIC).
101718 MW; 4939CD9B09B77208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Aryl-hydrocarbon interacting protein-like 1.
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PRO0515; TPR; 2.
PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; FALSE_NEG.
                                                                  PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
PROSITE; PS50166; IMPORTIN_B_NT; FALSE_NI
                                                                                                                                    HEAT 3
HEAT 4
HEAT 5
HEAT 6
HEAT 7
HEAT 9
                                                                                                                                                                                                                                                                                                        TLNCWMLSAFSRYARCLAEGHD 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20082814; PubMed=10615133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF180340; AAF26707.1; -.
InterPro; IPR001179; FKBP_PPlase.
InterPro; IPR001440; TPR.
                                           EMBL; Z99165; CAB16272.1; -. HSSP; Q92973; 1QBK.
                                                                                                                                                                                                                                                30.7%;
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Best Local Similarity 40.3.
Best Local Similarity 40.3.
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451
497
538
769
850
366
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Q9JLG9;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., 'VARIANT HIS-90, AND VARIANT LCA4 ARG-239.

MEDLINE-20082814; Pubmed-10615133;
A Sohocki M.M., Bowne S.J., Sullivan L.S., Blackshaw S., Cepko C.L.,
Payne A.M., Bhattacharya S.S., Khaliq S., Mehdi Q., Birch D.G.,
Harrison W.R., Elder F.F.B., Heckenlively J.R., Daiger S.P.;
"Mutations in a novel photoreceptor-pineal gene on 17p cause Leber congenital amaurosis.";
Nat. Genet. 24:79-83(2000).

I TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RETINA.

-1 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RETINA.

-1 TISSUE SPECIFICITY: A DISBASE CHARACTERIZED BY TOTAL BLINDNESS OR GREATLY IMPAIRED VISION WITH LOSS OF CENTRAL VISION.

-1 SIMILARITY: CONTAINS 2 THE REPRESTS.

-1 SIMILARITY: CONTAINS 2 THE REPARTS.

-1 SIMILARITY: CONTAINS 2 THE REPARTS.

-1 DATABASE: NAME-Mutations of the AIPLI gene.

NOTE-Retina International's Scientific Newsletter:

WWW-"http://www.retina-international.com/sci-news/aipllmut.htm".
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                  ij
                                                                                                                                          Score 53.5; DB 1; Length 328;
Pred. No. 4.1;
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C -> R (IN LCA4).
/FTId=VAR_010139.
; B116AA0724BAF9EA CRC64;
                                                                                  E9BC3A4084F64A0E CRC64;
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InterPro; IPR001179; FKBP_PPIase.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 2.
PROSITE; PS00454; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; FALSE_NEG.
Repeat; TPR repeat; Disease mutation; Vision.
DOMAIN 53 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aryl-hydrocarbon interacting protein-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AA
                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                       4 FWGDTLNCWMLSAFSRYARCLAEGHDGPT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H ^- Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF180472; AAF26708.1; -. Genew; HGNC:359; AIPL1.
                                                                                  38294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43596 MW;
                                                                                                                                          27.9%;
44.8%;
                                                                                                                                    Query Match 27.99
Best Local Similarity 44.8°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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53
230
264
328 AA;
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09NZN9;
DOMAIN
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SEQUENCE
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NATURE 351:761-765(1991).

NATURE 351:761-765(1991).

NATURE 351:761-765(1991).

THE PROPERTY OF TRIOLEIN.

C. I. CATALTION: THE EXTRACRELLULAR LIPASE PRODUCED BY G.CANDIDOM HUDROLYZES ALL ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH AFFINITY FOR TRIOLEIN.

C. I. CATALTION: THE EXTRACRELLY OF TRIOLEIN.

C. I. SAMILIANTY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

DR FIRST JOHOST: PRODUCING: CARBOXYLESTERASE B.1; I.

PROSITE: PSO0012: CARBOXYLESTERASE B.1; I.

PROSITE: PSO0013: CARBOXYLESTERASE B.1; I.

PROSITE: PSO0041: CARBOXYLESTERASE B.2; I.

R PROSITE: PROSITE: PROSITE B.2; I.

R PROSITE: PROSITE: PROSITE B.2; I.

R PROSITE: PROSITE: PROSITE 
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY TO CARBOXYLESTERASES.
MEDLINE-90328988; PubMed-2115773;
Slabas A.R., Windust J., Sidebottom C.M.;
"Does sequence similarity of human choline esterase, Torpedo acetylcholine esterase and Geotrichum candidum lipase reveal the active site serine residue?";
Blochem. J. 269:279-280(1990).
                                                                                                                                                                                                                                                                                                                                  Lipi.

Geotrichum candidum (Ospora lactis).

Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Galactomyces.

NCBL_TaxID=27317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 34614;
MEDLINE-90110016; PubMed-2481674;
Shimada Y., Sugihara A., Tominaga Y., Iizumi T., Tsunasawa S.;
"cDNA molecular cloning of Geotrichum candidum lipase.";
J. Blochem. 106:383-388(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-91287805; PubMed-2062369;
Schrag J.D., Li Y., Wu S., Cygler M.;
"Ser-His-Glu triad forms the catalytic site of the lipase from
               Query Match 27.9%; Score 53.5; DB 1; Length 384; Best Local Similarity 40.0%; Pred. No. 4.7; Matches 12; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Lipase 1 precursor (EC 3.1.1.3).
                                                                                                             4 FWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                        STANDARD;
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P17573;
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                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: PRESENT IN EGGS AND EARLY EMBRYOS BUT CANNOT
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE DETECTED IN LATE EMBRYOS. SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                               ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 26.6%; Score 51; DB 1; Length 418; I Similarity 44.0%; Pred. No. 11; 11; Conservative 3; Mismatches 11; Indels
                                                                                                    Score 52; DB 1; Length 563;
Pred. No. 11;
1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
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SEQUENCE 418 AA; 46772 MW; FEAUB7AIF8011E6A CRC64;
                                                                           61230 MW; 3B7327678CB7BAAA CRC64;
                                                                                                                                                                      1 LGTFWGDTL-----NCWMLSAFSRYARCLAEGHD 29
                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                             418 AA
                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P30274; IVIN.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                    27.18;
40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53745; CAA37775.1; -. PIR; S11678; S11678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SWART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
                                                                                                                              14; Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                            563 AA;
                                                                                                                  Similarity
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527
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P18606;
                                                                                                                                                                                                                                                                                                           Cyclin Al.
                                                                            SEQUENCE
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
MEDLINE-97426617; Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose H(2)0 = D-glucose 6-phosphate + D-glucose.
                                                                                                                                                                                                                                                                                                                                                                "Nucleotide Sequence, function, activation, and evolution of the cryptic asc operon of Escherichia coli K12.";
Mol. Biol. Evol. 9:688-706(1992).
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-1- FUNCTION: CAN HYDROLYZE SALICIN, CELLOBIOSE, AND PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 474;
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
EA -> GT (IN REF. 1).
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                                                                                              ASCB_ECOLI STANDARD; PRT; 474 AA. P24240; Q59375; P78104; O1-MAR-1992 (Rel. 21, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 6-phospho-beta-glucosidase ascB (EC 3.2.1.86) ASCB OR B2716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000650; GH_1; 1.
PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
Hydrolase; Glycosidase; Complete proteome.
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1larity 43.3%; Pred. No. 1
Conservative 3; Mismatch
356 FWPDTLEAFTGYALSDIAPCLSDLH 380
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InterPro; IPR001360; GH_1.
Pfam; PF00232; Glyco_hydro_1; 1.
PRINTS; PR00131; GLHYDRLASE1.
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EMBL; AE000355; AAC75758.1;
PIR; S27553; S27553.
PIR; C44070; C44070.
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                     B.G., Xu L.;
                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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Pfam; PF00008;
Pfam; PF00058;
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-89391964; PubMed-2789514;
Furuya M., Akashi S., Hirayama K.;
"The primary structure of human EGF produced by genetic engineering,
studied by high-performance tandem mass spectrometry.";
Biochem. Biophys. Res. Commun. 163:1100-1106(1989).
                                                                                                                                                                                                                   TISSUE-Kidney;
MEDLINE-87066721; PubMed-3491360;
MEDLINE-87066721; PubMed-3491360;
Bell G.I., Fong N.W., Stemplen M.M., Wormsted M.A., Caput D.,
Ku L., Urdea M.S., Rall L.B., Sanchez-Pescador R.;
"Human epidermal growth factor precursor: cDNA sequence, expression in vitro and gene organization.";
In vitro and gene organization.";
Nucleic Acids Res. 14:8427-8446(1986).
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                               21-JUL-1986 (Rel. 01, Created)
13-ANG-1987 (Rel. 05, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pro-epidermal growth factor precursor (EGF) [Contains: Epidermal
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 971-1023.
MEDLINE-77117897; Pubmed-300079;
Gregory H., Preston B.M.;
"The primary structure of human urogastrone.";
Int. J. Pept. Protein Res. 9:107-118(1977).
                     PRT; 1207 AA
         1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001336; EGF_11.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000033; Ldl_receptor_rep.
                                                                                                                            Pro-epidermal growth factor p
growth factor (Urogastrone)].
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                                                                            STANDARD;
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HSSP; P01132; 1EGF.
Genew; HGNC:3229; EGF.
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                                                                                                                                                          Homo sapiens (Human)
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                                                                           EGF_HUMAN
P01133;
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7, CALCIUM-BINDING (POTENTIAL).
8, CALCIUM-BINDING (POTENTIAL).
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                                                                      PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00012; BGF_1; 1.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01186; EGF_2; 7.
BGF_1; BGF_2; 7.
BGF_1; BGF_2; 3.
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EGF-LIKE 1.
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EGF-LIKE 4.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 9.
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL)
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Pred. No. 32;
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Pfam; PF00058; ldl_recept_b;
PR.NTS; PR00009; EGFTGF.
SMART; SM00179; EGF_CA; 2.
SMART; SM00001; EGF_like; 7.
SMART; SM00135; LY; 8.
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                                                                                                                                                                                                             MEDINE-90347835; PubMed-2384920;
Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
"Vital determinants of human immunodeficiancy virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398(1990).
                01-FEB-1991 (Rel. 17, Created)
1-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
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SIGNAL 1 29
                                                                                                                    Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11691;
                                                                                            glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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HIV; M38428; ENV$FF162.
InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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THE ALPHA CHAIN CONTAINS THE GUANINE NUCLECTIDE BINDING SITE.
-1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-74-0R23-1A;
MEDLINE-97432794; PubMed-9286674;
Baasiri R.A., Lu X., Rowley P.S., Turner G.E., Borkovich K.A.;
"Overlapping functions for two G protein alpha subunits in Neurospora
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Identification of a G protein alpha subunit from Neurospora crassa
that is a member of the [Idmilly],
J. Biol. Chem. 268:14805-14811(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crassa.";
Genetics 147:137-145(1997).
Genetics 147:137-145(1997).
- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSHEMBRANE SIGNALING SYSTEMS.
                                                                                    GBA2_NEUCR STANDARD; PRT; 355 AA.
005424; Q9URKO;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein alpha-2 subunit (GP2-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
                                                                                                                                                                                                                          Eukaryota; Fung1; Ascomycota; Pez1zomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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EL -> DV (IN REF. 2).
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Prima; Pr00503; G-alpha; 1.
PRINTS; PR001318; GPROTEINN.
Probom; PD000281; Gprotein_alpha; 1.
SMARR; SM0275; G-alpha; 1.
Probom; Proding; Transducer; Multigene family.
NP_BIND:
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MEDLINE-93315452; PubMed-8325859;
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355 AA; 41361 MW;
841 SMYARCISEGEDATCO 856
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11; Conservative
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ENV_HV1S1
ID ENV_HV1S1
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                          Gaps
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15-UIN-2002 (Rel. 41, Last annotation update)
Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
(Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5"'-
Pl,P4-tetraphosphate pyrophosphohydrolase).
                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
[Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5"'-
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                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                       Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
       DB 1; Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 282;
Pred. No. 14;
2; Mismatches 8; Indels
      Score 49.5; DB 1; Length 8 Pred. No. 36; 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 AA; 30631 MW; 7F83BE3404103374 CRC64;
                                                                                                                                                                                                                                                                                                                                       H(2)O = 2 ADP.
-!- SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
                                                         4 FWGDTLNCWM-----LSAFSRYARCLAEGHD 29
                                                                                                                 282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .282 AA
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR004844; S/T_phosphtse.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S/T_phosphtse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004617; ApaH.
InterPro; IPR004843; M-ppestrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY028370; AAK27390.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO0668; apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.5%;
30.2%;
      25.8%;
33.3%;
Query Match
Best Local Similarity 33.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000252;
                                                                                                                                                                                                                                     NCBI_TaxID=13373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
APAH_BURPS
ID APAH_BURPS
AC 069115;
                                                                                                                 APAH_BURMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                              DeShazer D., Brett P.J., Woods D.E.;
"The type II O-antigen molety of Burkholderia pseudomallei
lipopolysaccharide is required for serum resistance and virulence.";
Submitted (MAY.1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Hydrolyzes diadenosine 5',5"'-P1,P4-tetraphosphate to
yield ADP (EF similarity).
-!- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
H(2)O = 2 ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-CCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidase E (EC 3.4...-) (Alpha-aspartyl dipeptidase) (Asp-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the Escherichia coll genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Protecbacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 WRDTLRSLYGNDPNCWSPDLKHADRLRVAFNAFTRIRFCTPEG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 WGDTL-----NCW------ALSAFSRYARCLAEG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 AA; 30609 MW; 5D8BF833C5C27F44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE AP4A HYDROLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 49; DB 1; 30.2%; Pred. No. 14; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004617; ApaH.
InterPro; IPR004843; Mrpestrase.
InterPro; IPR004644; S/T phosphtse.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S/T_phosphtse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dipeptidase).
PEPE OR B4021 OR 25612 OR ECS4939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1555;
MEDLINE-94089392; Pubmed-8265357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF064070; AAD05453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIGRFAMS; TIGR00668; apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 30.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                      NCBI_TaxID=28450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000252;
                                                                                                                                                                                                         STRAIN-1026b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daniels D.L.
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Meijer W.J.J., Horcajadas J.A., Salas M.;
"The phi29 family of phages.";
                                                                                                                                                                                                                                                                                                                                       RESULT 14
AGRI_RAT
                                                                                                                                                                                                                                               Matches
               & F F C C C C C C C C F F F S
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                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                          Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakwa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterchemorrhagic Escherichia coli O15:H7 and genomic comparison with a laboratory strain K-12."; DNA Res R. 11-22(2001).
                                                                                                                                                                                                                                                                                  residues. May play a role in allowing the cell to use peptide aspartate to spare carbon otherwise required for the synthesis of the aspartate family of amino acids.
SUBCELLUIAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                            Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hectt J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no RNA stage; Caudovirales; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%; Score 48; DB 1; Length 229; llarity 37.0%; Pred. No. 16; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24570 MW; 53D4D8395DFC63FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine protease; Dipeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 DTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S51.001; --
EcoGene; EG11920; pepE.
InterPro; IPR005320; Peptidase_S51.
Pfam; PF03575; Peptidase_S51; 1.
                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000475; AAC76991.1; -. EMBL; AE005534; AAC59213.1; -. EMBL; AP002567; BAB38362.1; -. HSSP; P36936; 1FYE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00006; AAC43115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterlophage GA-1.
Viruses; dsDNA viruses,
phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major head protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-12345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEAD_BPGA1
Q9F2W7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Neurosci. 12:3535-3544 (1992).

-!- FUNCTION: COMPONENT OF THE BASAL LAMINA THAT CAUSES THE AGGREGATION OF AGETYLCHOLINE RECEPTORS AND ACETYLCHOLINE RESERVED ON THE SURFACE OF MUSCUE FIBERS OF THE NEUROMUSCULAR JUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: SYNAPTIC BASAL LAMINA AT THE NEUROMUSCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: CONTAINS 9 KAZAL-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 LAMININ EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-i- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-18 OR MET-24 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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-i- DEVELOPMENTAL STAGE: MORE ABUNDANT EARLY IN DEVELOPMENT.
-i- PTM: CONTAINS HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND
LINKED OLIGOSACCHARIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Embryonic spinal cord;
MEDILINE-9122570; PubMed-1851019;
RUPP F., Payan D.G., Magall-Solc C., Cowan D.M., Scheller R.H.;
"Structure and expression of a rat agrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER ACETYLCHOLINE RECEPTOR CLUSTERING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; Score 48; DB 1; Length 472; 33.3%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X96987; CAC21529.1; -.
SEQUENCE 472 AA; 53022 MW; 3104821153B1C4C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25304; Q63034; PRT; 1909 AA. P25304; Q63034; Q1-MAY-1992 (Rel. 22, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 GMYWNYLHVWQVLSTSRFANAVA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GTFWGDTLNCWMLSAFSRYARCLA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 33.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 6:811-823(1991).
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PPK_PSEAE STANDARD; PRT; 690 AA.
095646; 024816;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
Polyphosphate kiase (EC 2.7.4.1) (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase).
                    POTENTIAL.
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STRAIN-8830;
MEDDLINE-9240432: PubWed-10224002;
Zago A., Chuganl S., Chakrabarty A.M.;
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Best Local Similarity 39.3%;
Matches 11; Conservative
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
                                                                                                      EMBL; M64780; AAA40702.1; ALT_INIT.

EMBL; M64780; AAA40702.1; ALT_INIT.

EMBL; M64780; AAA40702.1; ALT_INIT.

EMBL; M64780; AAA40702.1; ALT_INIT.

EMBL; AA823326.1; ...

EMBL; AA80399; AGRT.

IN THEAPTO; IPRO01361; EGF-11ke.

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IN THEAPTO; IPRO01361; EGF-11ke.

IN THEAPTO; IPRO01361; EAAA1_Inhib.

IN THEAPTO; IPRO01391; Laminin_GF.

IN THEAPTO; IPRO01391; Laminin_GF.

IN THEAPTO; IPRO01390; Kazal.

PR Fam; PF00005; Kazal.

PR Fam; PF00005; Kazal.

PR Fam; PF00005; Kazal.

PR Fam; PF00005; Kazal.

PR Fam; PF00006; Kazal.

PR FAMT; SW0001; EGF-11ke; 4.

SWART; SW00020; EGF-11ke; 4.

SWART; SW00206; EAAG.

SWART; SW00206; EGF-1; 1.

PR SWART; SW00206; EGF-1; 1.

PR SWART; SW00206; EGF-1; 1.

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PR SWART; SW00206; EGF-1;
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EGF-LIKE 4.
LAMININ G-LIKE 3.
SER/THR-RICH.
SER/THR-RICH.
POTENTIAL.
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RAZAL-LIKE 1.
RAZAL-LIKE 2.
RAZAL-LIKE 3.
RAZAL-LIKE 4.
RAZAL-LIKE 5.
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RAZAL-LIKE 6.
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RAZAL-LIKE 7.
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EGF-LIKE 3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Catalyzes the reversible transfer of the terminal phosphate of ATP to form a long-chain polyphosephate (pD1yP).
-i- CATALYZIC ACTIVITY: ATP + [phosphate](N) = ADP + (phosphate)(N+1).
-i- PTM: An intermediate of this reaction is the autophosphate)(N+1).
-i- PTM: An which a phosphate is covalently linked to histidine residues through a N-P bond (By similarity).
-i- SIMILARITY: BELONGS TO THE POLYPHOSPHATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; iProvoss; 1.
Pfam; PF02503; PP_kinase; 1.
Transferase; Phosphorylation; Complete proteome.
ACT_SITE 435 435 FORMS THE PHOSPHOHISTIDINE INTERMEDIATE (BY SIMILARITY).

ANA FORMS THE PHOSPHOHISTIDINE INTERMEDIATE FORMS THE PHOSPHOHISTIDINE INTERMEDIATE
                                                                                                                                                                                                         STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
StOVEC C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Santh K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"Cloning and characterization of polyphosphate kinase and exopolyphosphatase genes from Pseudomonas aeruginosa 8830."; Appl. Environ. Microbiol. 65:2065-2071(1999).
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7F215EDD7F35742E CRC64;
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Pred. No. 64;
3; Mismatches
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Best Local Similarity 32.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                              SEQUENCE FROM N.A.
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    RRITER RR
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Search completed: May 29, 2003, 15:43:36 Job time : 24 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 29, 2003, 15:41:05; Search time 40 Seconds (without alignments) 79:311 Million cell updates/sec

US-09-989-481-4 192 1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues parched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	•	
SUMM	T38539 D70760 T52574 T39197 C87318 G87668 T01864 S41090 ACGUGC SC4248 S24249 S24249	\$24254 \$24253 \$24254 \$24247 \$685355 \$11678 \$71678 \$71678 \$71675 \$71678 \$
DB	000000000000000	ичичичичичичичи
% Query Match Length	910 6233 8444 2555 5433 11563 101 101	109 1109 1113 1113 373 474 474 474 474 1207 537 537 1207 1207 1207 1207 1207 1207 1207 120
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29.4%; Score 56.5; DB 2; Length 223;

Query Match

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30	33	3.5	36	37	36	4 4	42	43	44	45

### ALIGNMENTS

RESULT 1  TRESULT 1999  TRESULT 1999 #:sequence_revision 03-Dec-1999 #text_change 03-Dec-1999  C; Secession: T38539  TRESULT 1997  TRESULT 1997  TRESULT 1997  TRESULT 1997  TRESULT 1997  TRESULT 1997  TRESULT 1995  TRESULT 1996  TRESULT 1996
Query Match 30.7%; Score 59; DB 2; Length 910; Best Local Similarity 40.9%; Pred. No. 3.7; Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 8 TLNCWML&AFSRYARCLAEGHD 29  :      :         Db 473 TITCWTLGRYSKWASCLESEED 494
RESULT 2 D70760 hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C; Accession: D70760 R; Colonor, R: Parsch, R; Parkhill, J; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R: Davies, R.; Pevlin, X.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998 A; Authors: Squares, R.; Sulston, J.E; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A;0500; MuID: 98295987; PMID: 9634230 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-223 <col/> A; Cross-references: GE: Z74025; GB: All23456; NID: q3261586; PIDN: CAA98415.1; PID: e12999 A; Experimental source: strain H37RV C; Genetics: A; Gene: Rv2014

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Gaps

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C; Accession: G87668
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B; Laub, M.T.; DeBoy, R.T.; Dodson, R.D.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87318
A;Extus: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: G87668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <STO>
A;Cross-references: GB:AE005673; NID:g13425093; PIDN:AAK25347.1; GSPDB:GN00148
                                                                                                                                                                                           A;Cross-references: GB:AE005673; NID:913421749; PIDN:AAK22543.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein CC3385 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T7M24.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
C;Accession: T01864
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                                                                                                                                                                                                                                                                                                    Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T01864
R; Harmon, G; Langston, Y; Stoneking, T; Drone, K; Ames, M. submitted to the EMBL Data Library, July 1998
A; Description: The sequence of Arabidopsis thaliana T7M24.
A; Reference number: Z14448
A; Accession: T01864
A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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21;
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                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 2
Pred. No. 9.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2
                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:|:
|144 FWGETI-----SRTLNOAAEGHADPT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 FWGDTLNCWMLSAFSRYARCLAEGHDGPT 32
                                                                                                                                                                                                                                                                                                         Score 54;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4
A;Introns: 92/3; 105/2; 152/3; 268/1; 381/3
A;Note: T7M24.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AF077408; NID:qi
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                301 GDILSCWKLGAVPRYS 316
                                                                                                                                                                                                                                                                                                                                                                                                    6 GDTLNCWMLSAFSRYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.1%;
34.5%;
                                                                                                                                                                                                                                                                                                         28.1%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.1%;
Best Local Similarity 41.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                 Query Match 28.1
Best Local Similarity 56.2
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-533 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CC3385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: C87318
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                               Rikohler, C.; Merkle, T.; Neuhaus, G.
Plant J. 18, 97-104, 1999
A;Title: Characterisation of a novel gene family of putative cyclic nucleotide- and calm
A;Reference number: 226120
                                                                                                                                                                                                                                                   cyclic nucleotide and calmodulin-regulated ion channel [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yeast atp12 protein precursor homolog - fission yeast (Schizosaccharomyces pombe) (5)Species: Schizosaccharomyces pombe (5)Species: Schizosaccharomyces pombe (5)Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 (5)Accession: T33197
R;Wedler, H.; Duesterhoeft, A.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G. A;Wedler, H.; Duesterhoeft, A.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G. A;Accession: T39197
A;Accession: T39197
A;Accession: T39197
A;Accession: T39197
A;Accession: J-287 cwED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:AL121764; PIDN:CAB57430.1; GSPDB:GN00066; SPDB:SPAC9.12c
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                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C;Accession: T52574
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                              Indels
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                           6
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5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ A; Modecule type: mRNA RNA Residues: 1-694 < RCH3. Cross-references: EMBL:Y17912; PIDN:CAB40129.1 C: Experimental source: cultivar Columbia A; Genetics: A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 2;
Pred. No. 10;
                                                                                                        Pred. No. 2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                            4 FWGDT -- LNCWMLSAFSRYARCLAEGHDGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Experimental source: strain 972h-; cosmid c9 (Genetics: A)Gene: SPDB:SPAC9.12c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 WGDTLNCWMLSAFSRYARC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%;
35.9%;
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Best Local Similarity 47.4%;
Matches 9; Conservative 3
1larity 46.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GT-FWGDTLN-----
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Matches 14; Conserv
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid
F; 1-19/Domain: signal sequence *status predicted <SIG>
F; 1-19/Domain: signal sequence *status predicted <SIG>
F; 20-563/Product: triacylglycerol lipase *status experimental <MAT>
F; 23-560/Domain: cholinesterase homology <CHE>
F; 23-238/Region: interfactal lipid recognition (GXSKG) motif
F; 20/Modified site: Pyrrollidone carboxylic acid (Gln) (in mature form) *status experif: 80-124, 295-307/Disulfide bonds: *status predicted
F; 236/Active site: Ser *status predicted
F; 302,383/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S24248
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B A;Recence number: S24247
A;Accession: S24248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Giasson, L.; Kronstad, J.W.
Genetics 141, 491-501, 1995
A;Title: Mutations in the mypl gene of Ustilago maydis attenuate mycelial growth and
A;Reference number: S58775; MUID:96109597; PMID:8647387
A;Accession: S58775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mypl protein - smut fungus (Ustilago maydis)
C;Species: Ustilago maydis (corn smut)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (VH26) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb_1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: EMBL:L33919; NID:g886415; PIDN:AAC37439.1; PID:g886416
C;Genetics:
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A;Residues: 1-90 <STE>
A;Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID:g38396
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1150;
                                                                                                                                                                                                                                                                                                                                                Length 563;
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                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 LGTFHGSDLLFQYYAGPWSSSAYRRYFISFANHHD 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LGTFWGLTL-----NCWMLSAFSRYARCLAEGHD 29
                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                             Score 52; DB pred. No. 22; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 53;
7; Mismatches
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714 IGTFW-LSRNAWILA--TRHGHLLSPGH 738
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Pred. No.
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39.3%;
                                                                                                                                                                                                                                                                                                                                             Query Match 27.1%;
Best Local Similarity 40.0%;
Matches 14; Conservative
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Best Local Similarity 52.2'
Matches 12; Conservative
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Best Local Similarity 39.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1150 <GIA>
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A; Residues: 1-544 CBERD
A; Cross-references: 68:002622; NID:9409275; PIDN:AAA03435.1; PID:9409276
A; Experimental source: ATCC 34614
A; Bxperimental source: ATCC 34614
A; Note: only the translation of the mature protein is shown
C; Genetics:
A; Genetics:
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic aci
F; 24-541/Domain: cholinesterase, homology C; Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic aci
F; 24-541/Domain: cholinesterase homology C; Keywords: interfacial lipid recognition (GXSXC) motif
F; 215-219/Region: interfacial lipid recognition (GXSXC) motif
F; 1/Modified site: pyrrolidone carboxylic acid (GIn) *status predicted
F; 61-105,276-288/Disulfide bonds: *status predicted
                                                                                                                                                                                                                   Naternate names: lipeae
C;Species: Geotrichum candidum
C;Species: Thomada, Y.; Sugihara, A.; Tominaga, Y.
A;Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum
A;Reference number: PN0492; MUID:93380907; PMID:8370674
A;Accession: PN0492
A;Residues: DNA
A;Residues: 1-563 <NAG>
A;Note: the translation of residues 31-550 and the corresponding nucleotide sequence are
B;Shimada, Y.; Sugihara, A.; Tominaga, Y.; Iizumi, T.; Tsunasawa, S.
A;Title: CDNA molecular cloning of Geotrichum candidum lipase.
A;Reference number: J00022; MUID:90110016; PMID:2481674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ester
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A; Note: sequences of several small peptides were also determined
C; Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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  Gaps
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;283,364/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 21;
1; Mismatches 14; Indels
     Indels
  13;
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  Mismatches
                                                                                      145 LGOIXKESVNYWMSHRTLKFARHLVRGRD 173
                                                     1 LGTFWGDTLNCWMLSAFSRYARCLAEGHD 29
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Best Local Similarity 40.0
Matches 14; Conservative
10; Conservative
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A; Residues: 1-563 <SHI>
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Matches
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completed: May 29, 2003, 15:45:53
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Query Match
Best Local Similarity
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                                      C;Species: Homo sapiens (man)
C;Date: 19:Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 19:Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: $24257
R;Stewart, AK.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel A;Accession: $24247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (VH26-DN1-DXP1-JH4) - human C.Species: Homo sapiens (man) (Jaceies: Homo sapiens (man) (Jaceies: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997 (Jacession: S2424) (Jaceies Jaceies Jacei
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A; Molecule type: DNA
A; Residues: 1-105 <STE>
A; Cross-references: EMBL:X67070
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 10-92/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region (VH26-DXP1-JH4) - human
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LGTAWGVPETLLCSLWFTFSSYA 28
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A; Status: preliminary
A; Molecule type: DNA
Residues: 1-109 <STES
A; Cross-references: EMBL:X67062
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A; Molecule type: DNA
A; Residues: 1-101 <STE>
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C; Species: Homo sapiens (man)
C; Sate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Accession: S24253
R; Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the Embi. Data Library, June 1992
A; Description: A single VH gene predominates in the rearranged and expressee
A; Reference number: S24247
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A; Status: preliminary
A; Molecule type: DAR
A; Cross-references: EMBL: X67061
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 12-94/Domain: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                        Score 51; DB 2;
Pred. No. 5.7;
                                                                                                                                                                        2; Mismatches
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                                                                                                                 26.6%;
52.2%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 29, 2003, 15:45:06 ; Search time 46 Seconds Run on:

(without alignments)
72.617 Million cell updates/sec

US-09-989-481-4 192 1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33 Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

383519 seqs, 101223694 residues arched:

383519 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published\_Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 75, Appl			Sequence 78, Appl	72, 1	73, 1	77, 1	1081	Sequence 83, Appl	Sequence 10270, A	Sequence 2, Appl1	Sequence 80, Appl	.:	Sequence 34, Appl	Sequence 39145, A	Sequence 11786, A	Sequence 24, Appl	Sequence 41036, A	Sequence 3606, Ap
ID	US-09-765-061B-75	US-09-765-061B-76	US-09-765-061B-74	US-09-765-061B-78	US-09-765-061B-72	US-09-765-061B-73	US-09-765-061B-77	US-09-764-891-3081	0 US-09-908-711-83	0 US-09-815-242-10270	0 US-09-476-242-2	US-09-851-138-80	US-10-210-296-102	US-10-016-283-34	0 US-09-864-761-39145	0 US-09-815-242-11786	US-10-055-364-24	0 US-09-864-761-41036	US-09-738-626-3606
gth DB	328 9	328 9	372 9	372 9	384 9	384 9	392 9	56 9	56 10	474 10	847 10	113 9	526 9	1940 9	84 10	467 10	865 9	107 1(	384 9
% Query Match Length DB	9.4	17.9	17.9	9.7	9.7			26.6	9.9			5.0			7.4.7		14.7	4.2	4.2
Qu Score Ma	56.5	53.5	53.5	53.5	53.5	53.5	53.5	51 2	51 2	51 2	49.5	48	48	48	47.5		47.5 2	46.5 2	46.5
Result No.	1	7	m	4	S	س	7	8	6	10	11	12	13	14	15	16	17	18	19

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Sequence 12845, A Sequence 3, Appl Sequence 183, Appl Sequence 14, Appl	Sequence 396, App Sequence 67, Appl Sequence 40394, A Sequence 132, App Sequence 3329, Ap	Sequence 3738, A Sequence 2, Appl1 Sequence 8, Appl1 Sequence 2, Appl1 Sequence 4, Appl1	Sequence 41463, A Sequence 4499, Ap Sequence 135, App Sequence 88, Appl Sequence 91, Appl Sequence 91, Appl	Sequence 59, Appl Sequence 119, App Sequence 78, Appl Sequence 484, Appl Sequence 6, Appl
10 US-09-815-242-12845 10 US-09-932-474-3 9 US-09-866-050A-183 9 US-09-924-097-14	9 US-09-866-050A-396 US-10-189-123-67 10 US-09-864-761-40394 10 US-09-113-459-132 10 US-09-815-242-5329 10 US-08-815-242-5329	10 US-09-864-761-37338 10 US-09-966-234-2 11 US-09-957-943-8 10 US-09-970-318-2 10 US-09-970-318-4	0000	10 US-09-350-874-59 9 US-09-791-932-119 9 US-09-851-138-78 10 US-09-925-297-484 9 US-10-202-676-6
421 421 716 925	1529 1529 67 235 421	49 114 114 201	68 177 199 199 211 261	270 323 113 211 228
24.2 24.2 24.2	24.2 23.7.2 23.7.7.5 7.7.5	223333 2333.44.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	23.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5	23.2 22.9 22.9 9.0 9.0
46.5 46.5 46.5 46.5	4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44444 888888	244444 24444 2. 2. 3. 444 2. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3.	44 4.5 44 44 44
22 23 23 23	22 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4	333 333 34 34	33 3 3 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5	4444 102643

#### ALIGNMENTS

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Sequence 75. Application US/09765061B
Publication No. US20030022165A1
GENERAL INFORMATION:
BAPLICANT: Board of Regents of the University of Texas System
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1 Photoreceptor-pineal gene
TITLE OF INVENTION: Neber congenital amaurosis (LCA4)
TITLE OF INVENTION: NUMBER: US/09/765,061B
CURRENT APPLICATION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 76, Application US/09765061B
PUBLICATION NO. US20030022165A1
GENERAL INFORMATION:
APPLICAMTS Board of Regents of the University of Texas System
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1 Photoreceptor-pineal gene
TITLE OF INVENTION: Leber congenital amaurosis (LCA4)
FILLE REFERENCE: 966.06/160TL
CURRENT APPLICATION NUMBER: US/09/765,061B
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; OTHER INFORMATION: COW AIPLI Protein
US-09-765-061B-75
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Best Local Similarity 43.37
Matches 13; Conservative
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US-09-765-061B-76
US-09-765-061B-75
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PRT
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Sequence 2. Application US/09765061B
Sequence 2. Application US/09765061B
Publication No. US20030022165A1
GENERAL INFORMATION:
BOARD OF Regents of the University of Texas System
APPLICANT: BOARD OF Regents of the University of Texas System
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1 Photoreceptor-pineal gene
TITLE OF INVENTION: leber congenital amaurosis (LCA4)
FILE REFERENCE: 96606/16UTL
CURRENT APPLICATION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 73, Application US/09765061B
Publication No. US20030022165A1
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Texas System
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1 Photoreceptor-pineal gene
TITLE OF INVENTION: leber congenital amaurosis (LCA4)
FILE REFERENCE: 96606/160TL
CURRENT APPLICATION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
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                                                                                                                              Gaps
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CTHER INFORMATION: Human AIPL1 Protein
NAME/RET: misc_feature
LOCATION: (322)..(322)
OTHER INFORMATION: Xaa represents any of the twenty amino acids US-09-765-061B-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 384;
                                                                                    Length 372;
                                                                                                                            Indels
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                                                                                                                            11;
                                                                                  27.9%; Score 53.5; DB 9;
40.0%; Pred. No. 10;
tive 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
; LOCATION: (1)..(372)
; OTHER INFORMATION: Squirrel Monkey AIPL1 Protein
US-09-765-061B-78
                                                                                                                                                                                             || ||:: : || | :|:| | ||:
87 FWCDTIHTGVYPILSRSLRQMAQGKD-PTE 115
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40.0%; Pred. No. 11;
tive 6; Mismatches
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; OTHER INFORMATION: Chimpanzee AIPL1 Protein US-09-765-061B-73
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Pred. No. 11;
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40.0%;
                                                               Query Match
Best Local Similarity 40.00
Local 12; Conservative
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Best Local Similarity 40.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-765-061B-73
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US-09-765-061B-72
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LENGTH: 384
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LENGTH: 384
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Publication No. US20030022165A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1
FILE OF INVENTION: Leber congenital amaurosis (LCA4)
FILE REPERBNCE: 96606/16UTL
CURRENT APPLICATION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Mutations in a No. US20030022165Alel Photoreceptor-pineal gene 17
TITLE OF INVENTION: Leber congenital amaurosis (LCA4)
FILE REFERENCE: 96606/16TL
CURRENT APPLICATION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 78
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Pred. No. 10;
6; Mismatches
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Pred. No. 9.1;
4; Mismatches
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; OTHER INFORMATION: Baboon AIPL1 Protein US-09-765-061B-74
                                                                                                                                                                   : NAME/KEY: PEPTIDE

: LOCATION: (1)..(328)

: OTHER INFORMATION: Mouse AIPL1 Protein
US-09-765-061B-76
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  2001-01-17
                   NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
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Best Local Similarity 40.0%;
Matches 12; Conservative
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Best Local Similarity 44.8%;
Matches 13; Conservative
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ORGANISM: Saimiri sciureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Papio anubis
                                                                                                                         ORGANISM: Mus musculus
  CURRENT FILING DATE:
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US-09-765-061B-78
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                                                                                  LENGIH: 328
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TYPE: PRT
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                                                                                                      TYPE: PRT
                                                                                                                                                 FEATURE:
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APPLICANT: Rosen et al. TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                           CURRENT APPLICATION NUMBER: US/09/908,711 CURRENT FILING DATE: 2001-07-20
                                                                                                                                                            PRIOR APPLICATION NUMBER: 0501/01360
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 0501/01344
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 05/764,892
PRIOR FILING DATE: 2001-01-17
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LICATION NUMBER: 09/764,874
LICATION NUMBER: 09/764,874
LICATION NUMBER: US01/01334
ING DATE: 2001-01-17
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LICATION NUMBER: US01/01349
.ING DATE: 2001-01-17
LICATION NUMBER: 09/764,902
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PLICATION NUMBER: 09/764,870
LING DATE: 2001-01-17
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APPLICATION WINDER: 09/764,882
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01347
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APPLICATION NUMBER: 09/764,868
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01312
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APPLICATION NUMBER: 09/764,905
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LICATION NUMBER: US01/01340
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LICATION NUMBER: US01/01320
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LICATION NUMBER: 09/764,853
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LICATION NUMBER: US01/01239
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APPLICATION NUMBER: US01/01341
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APPLICATION NUMBER: 09/764,856
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PPLICATION NUMBER: US01/01354
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ING DATE: 2001-01-17
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APPLICATION NUMBER: US01/01307
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APPLICATION NUMBER: 09/764,864
  Application US/09908711
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PPLICATION NUMBER:
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PRIOR
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TITLE OF INVENTION: Mutations in a No. US2003002165Alel Photoreceptor-pineal gene 17
TITLE OF INVENTION: Leber congenital amaurosis (LCA4)
FILE REFERENCE: 96606,16UTL
CURRENT APPLICATION NUMBER: US/09/765,061B
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
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; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3081
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    Gaps
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Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006

CURRENT PRPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

LENGTH: 56
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    Indels
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  11;
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Pred. No. 11;
6; Mismatches 11;
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; LOCATION: (1)..(392)

; CTHER INFORMATION: Rhesus Monkey AIPL1 Protein

US-09-765-061B-77
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                                         4 FWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
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57.9%;
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40.0%;
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12; Conservative
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ORGANISM: Macaca mulatta
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-764-891-3081
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Matches
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; ORGANISM: Human 1mmunodeficiency virus
US-09-476-242-2
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                                                                                                                                                 Sequence 2, Application US/09476242 Patent No. US20020146683A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MAERTENS, GEERT
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3'
Matches 11; Conservative
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                                                                                                                                                                                            GENERAL INFORMATION:
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US-09-851-138-80
                                                                                                                              US-09-476-242-2
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                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (12); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-711-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: X0, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKATYORES

TITLE OF INVENTION: PROKATYORES

CURRENT FILING DATE: 2001-03-21

PRIOR PELICATION NUMBER: 60/290, 48

PRIOR APPLICATION NUMBER: 60/200, 48

PRIOR APPLICATION NUMBER: 60/200, 727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-36

PRIOR FILING DATE: 2000-05-36

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-110-27

PRIOR FILING DATE: 2000-110-27

PRIOR FILING DATE: 2000-110-27

PRIOR FILING DATE: 2000-110-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27
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Pred. No. 3;
1; Mismatches 5; Indels
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3; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10270
LENGTH: 474
PRIOR FILING DATE: 2001-01-1/
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 83
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10270, Application US/09815242
Patent No. US20020061569Al
GENERAL INFORMATION:
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 57.9%;
Matches 11; Conservative
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1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30

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TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
RILING DATE: 09-May-2001
PRIOR APPLICATION NUMBER: 08/836,075
FILING DATE: <UNKnown>
APPLICATION NUMBER: P9 94870166.9
FILING DATE: <21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605 002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT APPLICATION NUMBER: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 847
                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 YWGNLLQYWIQELKNSAVSLFDAIAIAVAEGTD 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 FWGDTLNCWM-----LSAFSRYARCLAEGHD 29
                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 49.5; 1
Pred. No. 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: LAWSONIA INTRACELLUIARIS PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
FILE REFERENCE: PC10589A
CURRENT PAPLICATION NUMBER: US/10/210,296
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/689,065
PRIOR FILING DATE: 2000-10-12
SPRIOR FILING DATE: 2000-10-12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10.2
                                                                                                                                                                      4
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Patent No. US20020164702A1
Patent No. US20020164702A1
Patent No. US20020164702A1
Patent No. US20020164702A1
Patent Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/10/016, 283
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US/09/077, 955A
PRIOR FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 9; Length 1940; 3.9e+02;
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                                                                                                                         Length 113
                                                                                                                                                                    11; Indels
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                                                                                                                       Score 48; DB 9;
Pred. No. 17;
4; Mismatches 1:
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Pred. No. 93;
5; Mismatches 1
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                                                                                                                                                                                                            3 TFWGDTLNCWMLSAFSRYARCLAEGHDGPT 32
                                                                                                                                                                                                                                                 62 TSMGNTITCYV----KAMAACRAAGIDAPT 87
                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-851-138-80
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Pred. No.
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PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VEY. 2.0
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                                                                                                                                                                                                                                                                                                                                                         Sequence 102, Application US/10210296 Publication No. US20030021802A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CRCANISM: Lawsonia intracellularis US-10-210-296-102
                                                                                                                       ch 25.0%;
1 Similarity 36.7%;
11; Conservative
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Best Local Similarity 40.0%;
Matches 10; Conservative
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Best Local Similarity 39.3%;
Matches 11; Conservative
TYPE: amino acid
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Matches 11; Conserva
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; ORGANISM: Rattus sp.
US-10-016-283-34
                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-210-296-102
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                                                                                                                         Query Match
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6 GDTLN--CWMLSAFSRYARCLAEGHDGP 31

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84;	11;		
Length	6; Indels 11; Gaps		
DB 10;	9		
Score 47.5; 1 Pred. No. 15;	3; Mismatches	WARCLAEGHDG 30	KCHVEPHDG 68
Query Match 24.7%; Score 47.5; DB 10; Length 84; Best Local Similarity 33.3%; Pred. No. 15;	; Conservative	1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30	50 LDPFWAISCWKCHVEPHDG 68
Query Match Best Local S	Matches 10	0y 1	Dp 20

Search completed: May 29, 2003, 15:54:15 Job time : 48 secs

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TYPE: PRT
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                                                                                                                                                      (without alignments)
35.961 Million cell updates/sec
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                                                                                                                              May 29, 2003, 15:42:00 ; Search time 27 Seconds
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6 . Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                             192
1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
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US-08-368-803-7
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US-08-362-240A-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                            Scoring table:
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44444
7......4444
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                                                                                       OM protein
                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                            searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Sequence 5, Appl1 Sequence 78, Appl Patent No. 5223425 Sequence 44, Appl Patent No. 5223425

US-08-944-483-44

5223425-6 5223425-5

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Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08928862
Patent No. 6309877
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chau, Faymond M. W.
TITLE OF INVENTION: Isolation and Use of Motoneuronotrophic Factors
FILE REFERENCE: 15592-2
CURRENT APPLICATION NUMBER: US/08/928,862
CURRENT FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                 Sequence (
                                                                                                                              Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Steven A. Benner
STREET: 1501 NW 68th Terrace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                              US-08-190-802A-48
US-08-473-089-48
US-08-487-072A-48
US-08-08-06-659-107
US-08-906-616-107
US-08-917-795-107
US-08-317-795-107
US-09-012-431-107
US-09-012-692-107
US-09-012-692-107
US-09-012-692-107
US-09-014-431-107
US-09-014-613-107
US-09-014-613-107
US-09-014-613-107
US-09-004-731-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 192; DB 4; Best Local Similarity 100.0%; Pred. No. 2e-20; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                          US-08-749-699-13
US-09-004-729-13
US-09-004-731-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-14-375C-60
US-08-14-375C-60
; Sequence 60, Application US/08914375C
; Patent No. 6377893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-08-928-862-4
RESULT 1
US-08-928-862-4
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Length 1940;
       Score 48; DB 4; Length 113;
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 2;
Pred. No. 3.2e+02;
1; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
                                                    4; Mismatches
                                                                                                 3 TFWGDTLNCWMLSAFSRYARCLAEGHDGPT 32
                                                                                                                        62 TSMGNTITCYV----KAMAACRAAGIDAPT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 GHTYNNDCWRQQAECRQQRAIPPKHQGP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDION TIPE: DISKETCE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,271
ELLING DATE: 10-MAY-1996
CLASSIFCATION 435
PRIOR APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBERT J
REFIRENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 195A
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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APPLICANT: Valenzuela et al., David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/09077955A
Patent No. 6413740
                                                                                                                                                                                                                                                        Sequence 30, Application US/08644271
Patent No. 5814478
GENERAL INFORMATION:
  ch 25.0%;
1 Similarity 36.7%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.0%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1940 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: Rat Agrin
; LOCATION: 1...1940
; OTHER INFORMATION:
US-08-644-271-30
Query Match
Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Ta
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                        6-phospho-strand-glucosidase (E.C. 3.2.1.86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                             4; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDAPY disk
COMPUTER: IDAPY DISK
COMPUTER: IDA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FP95/04155
FILING DATE: 23 Oct 1995
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
FILING DATE: 21 Oct 1994
FILING DATE: 22 Uni 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 4
Pred. No. 24;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: ascb_ecol1; SEQUENCE DESCRIPTION: SEQ ID NO: 60: US-08-914-375C-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING LALL.
TORNEY/AGENT INFORMATIC...
NAME: KAMMERER, PATRICIA A.
NAME: TONNERER: 29,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: ARNOLD, WHITE & DURKEE I: P.O. BOX 4433 HOUSTON
                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli
                            TELECOMMUNICATION INFORMATION
                                               TELEPHONE: 352 392 7773
TELEFAX: 352 310 462
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
       CLASSIFICATION: 702/20
                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,777:
REFERENCE/DOCKET NUMBER: II
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIAL STATE: TEAL COUNTRY: USA 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-836-075A-80
                                                                                                                                                                                                                                                                              FEATURE
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Gaps

Indels

Length 243;

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APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: E98-031-3
CURRENT PAPLICATION NUMBER: US/09/540,245A
CURRENT PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/055,544
PRIOR APPLICATION NUMBER: 60/055,544
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1997-11-14
PRIOR PELICATION NUMBER: 60/081,057
SPRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
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Patent No. 6270995
GENERAL INFORMATION:
APPLICANT: GOOdman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 46.5; D
50.0%; Pred. No. 49;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                Score 46.5;
Pred. No. 49
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CURRENT FILING DATE: 2000-03-31
PRICA PLICATION NUMBER: 09/191,647
PRICE FILING DATE: 1998-11-13
PRICE APPLICATION NUMBER: 60/081,057
  CURRENT APPLICATION NUMBER: US/09/191,647
                  CURRENT FILING DARE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DARE: 1997-11-14
EARLIER FILING DARE: 1998-04-07
NUMBER OF SEQ ID NOS: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-540-245A-14
; Sequence 14, Application US/09540245A
; Patent No. 6270984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 CLPINAFSYSCKCL-EGHGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 CLPINAFSYSCKCL-EGHGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                                                                                   24.2%;
50.0%;
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Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: mouse
US-09-540-245A-14
                                                                                                                                                                                                                                                                          ; ORGANISM: mouse US-09-191-647-14
                                                                                                                                                                                                 SEQ ID NO 14
LENGTH: 243
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-540-153-14
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APPLICANT: Patience, Clive
TITLE OF INVENTION: Swine Gamma Herpesvirus DNA and Methods of Use
FILE REFERENCE: 61750-299
CURRENT APPLICATION NUMBER: US/09/612,204B
CURRENT APPLICATION NUMBER: US. 60/142,736
PRIOR FILING DATE: 1999-07-08
PRIOR PELING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
LENGTH: 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Deduced amino OTHER INFORMATION: acid sequence of porcine gamma herpesvirus gpB COTHER INFORMATION: gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
2
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 24.7%; Score 47.5; DB 4; Length 865; Best Local Similarity 39.1%; Pred. No. 1.5e+02; Matches 9; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goodman, Corey
APPLICANT: K1d, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TILLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.0%; Score 48; DB 4;
Best Local Similarity 39.3%; Pred. No. 3.2e+02;
Matches 11; Conservative 1; Mismatches 14
               FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/07,955A
CURRENT FILING DATE: 1998-09-10
EARLIER PELING DATE: 1996-10-13
EARLIER PILING DATE: 1996-12-13
EARLIER PILING DATE: 1996-12-13
EARLIER PILING DATE: 1996-05-10
EARLIER PILING DATE: 1996-05-10
EARLIER FILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE PATENTY NUMBER: 60/008,657
EARLIER FILING DATE: 1995-12-15
SOFTWARE: PATENTY NUMBER: 00/008,657
EARLIER FILING DATE: 1995-12-15
SOFTWARE: PATENTY NUMBER: 00/008,657
EARLIER FILING DATE: 1995-12-15
SOFTWARE: PATENTY NEW CO. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 GHTYNNDCWRQQAECRQQRAIPPKHQGP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GDTLN--CWMLSAFSRYARCLAEGHDGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GWFWGSYRRTTVNCELMDMFAR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GTFWGD----TLNCWMLSAFSR 19
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; Sequence 14, Application US/09191647
; Patent No. 6046015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-077-955-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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                                                                                                      Length 1525;
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APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Brose, Marc
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 1097-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR PILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Goodman,
TILE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR PILING DATE: 1998-11-13
PRIOR PELICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                    Score 46.5; DB 3;
Pred. No. 3.9e+02;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; Score 46.5; DB 4; 50.0%; Pred. No. 3.9e+02; tive 3; Mismatches 6;
                                                                                                                                                                                                         1381 CLPINAFSYSCKCL-EGHGG 1399
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                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09540245A Patent No. 6270984
                                                                                                                                                                                  11 CWMLSAFSRYARCLAEGHDG 30
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                                                                                                    24.2%;
50.0%;
                                                                                                    Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Goodman, Corey
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SOFTWARE: Patentin V
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Goodman
                    ; TYPE: PRT
; ORGANISM: human
US-09-191-647-2
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ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 1525
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LENGTH: 1525
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 183, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Steeman, Matthew
APPLICANT: Ornsit, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions
FILE REFERENCE: 11000.1011c1
CURRENT PILLOR DINOR: 318
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SSOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 183
LENGTH: 771
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Patent No. 6046015

GENERAL INFORMATION:

APPLICANT: GOOdenn, Corey

APPLICANT: GOOdenn, Corey

APPLICANT: Brose, Katja

APPLICANT: Tessler-Lavigne, Marc

TITLE OF INVENTION: Modulating Robo: Ligand Interactions

FILE REFERENCE: B98-031-3

CURRENT APPLICATION NUMBER: US/09/191,647

CURRENT FILING DATE: 1998-11-14

EARLIER PILING DATE: 1997-11-14

EARLIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 14

SOFTWARRE: Patentin Ver. 2.0
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                              Score 46.5;
Pred. No. 49
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                                                                                                                                                                              24.2%;
50.0%;
  1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.2%;
Best Local Similarity 50.0%;
Matches 10; Conservative
                                       Patentin Ver. 2.0
                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (717)...(717)
US-09-188-930-183
PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
                                                                                                ; TYPE: PRT
; ORGANISM: mouse
US-09-540-153-14
                                                                                                                                                                                                                                                                                                                                                      RESULT 10 .
US-09-188-930-183
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ORGANISM: Rat
                                                       SEQ ID NO 14
LENGTH: 243
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Patent No. 5994070
CENERAL INFORMATION:
APPLICANT: Streul1, Michel
TITLE OF INVENTION: No. 5994070e1 TRIO Molecules and Uses Related Thereto NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION GENOMIC PPO CLONES
TITLE OF INVENTION: GENOMIC PPO CLONES
TITLE OF INVENTION: GENOMIC PPO CLONES
FILE REFERENCE: 57072-PCT-US
CURRENT APPLICATION NUMBER: US/09/129,030A
EARLIER APPLICATION NUMBER: AU PN7856
EARLIER FILING DATE: 1996-08-16
EARLIER FILING DATE: 1996-03-16
EARLIER FILING DATE: 1996-03-16
EARLIER FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 28
LENGTH: 196
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                                                     Gaps
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ch 24.2%; Score 46.5; DB 4; Length 1525; Similarity 50.0%; Pred. No. 3.9e+02; 10; Conservative 3; Mismatches 6; Indels 1
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,267
FILING DATE: 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CWMLSAFSRY----ARCLAEGHDGPT 32
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-010
                                                                                                                                                                                                                                               Sequence 28, Application US/09129030A Patent No. 624221
GENERAL INFORMATION:
                                                                                                                    1381 CLPINAFSYSCKCL-EGHGG 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,214
FILING DATE: 27 MARCH (1996)
ATTORNEY/AGENT INFORMATION:
                                                                                          11 CWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.79
Matches 11; Conservative
    Query Match
Best Local Similarity
Matches 10; Conserv
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US-09-129-030-28
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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192
1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTO 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*
15: /SIDS2/gcgdata/geneseq/geneseq-embl/AA1994.DAT:\*
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/SIDS2/gcgdata/genesed/genesedp-emb1/Aa1989 /SIDS2/gcgdata/genesed/genesegp-emb1/Aa1990 /SIDS2/gcgdata/geneseq/genesegp-emb1/Aa1991. /SIDS2/gcgdata/geneseg/genesegp-emb1/Aa1992. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description		Human MNTF1-F6 pro	Comamonas testoste	Human diagnostic a	Herbicidally activ	Hepatitis B virus	Human protein sequ	Novel human diagno	Gene product with	Human ovarian anti	Human reproductive
		Ω		AAW59046	AAW90949	AAU19525	ABB93813	AAB23939	AAB94802	ABG25667	AAR10330	ABG60253	AAM94423
		DB	1 1	13	21	22	23	21	22	22	12	22	22
		Match Length DB		33	584	227	694	326	384	794	563	56	26
æ	Query	Match		100.0	29.4	28.9	28.6	27.9	27.9	27.6	27.1	26.6	26.6
		Score	1 1 1 1	192	56.5	55.5	55	53.5	53.5	53	52	51	51
	Result	No.		<b>-</b>	7	m	4	'n	<b>.</b>	7	80	6	10

(KMBI-) KM BIOTECH INC

Chau RMW;

WPI; 1998-230703/20. N-PSDB; AAV1174E.

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Novel ovarian rela Escherichia coli 6 E. coli cellular p Human protelin SEQ Amino acid sequenc Human precursor pr Human protein SEQ Novel human diagno	22/DND1 51011) 51011) 51011) 51011 5	. F6; human; axon regeneration; Wound healing; scar tissue;
	AAB68590 AAB63489 ABB63489 ABB63101 AAXY9773 AAXY96710 AAB66410 AAB66410 AAB64425 AAW68415 AAW68415 AAW68415 AAW6666 AAB630165 AAB630166 AAB630166 AAB630166 AAB630166 AAB630166 AAB630166 AAM72017	ALIGNMENTS AA. F-1; MNTF1- disease;
.6 466 .6 474 .6 1207 .6 1222 .6 1222 .6 1222 .6 1225	726 22 726 23 726 23 8 8 842 8 8 8 82 8 9 8 82 9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Pro ein ein fa e; -us -us -000
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		RESULT 1 AAW59046 ID AAW59046 ID AAW SOUGH XX AAW XX AAW XX HUM XX MOT X

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WO200162927-A2.
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24-FEB-2000;
24-FEB-2000;
                                                                                        04-DEC-2001
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5-MAY-2000;
                                                                                                                                                                                                                                                                                                                  4-FEB-2000
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                                                                  AAU19525;
                                                                                                                                                                                           Ношо
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                            This sequence, represents a fragment of a novel human motoneurotrophic factor, MNTP1-F6. Such factors are used to promote regeneration of the axon of a motoneurone, to diagnose and treat motoneurone disease in a mammal or to accelerate wound healing whilst concomitantly minimising or inhibiting scar tissue and/or keloid formation in an area associated with a wound. For promoting axonal regeneration, the polypeptide is administered at a concentration of 5 ng-50 mg, whereas for inhibiting hereditary motoneurone disease, the dosage is 5-100 (especially 30-50)ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structural gene and a regulator gene of phenol hydroxylase of Comamonas testosterron1 R5 - used for decomposing phenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel microbe for decomposing phenol which
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Motoneurotrophic factor MNTF1-F3 and MNTF1-F6 - useful for motoneuron regeneration, diagnosing or treating motoneuron disease and to accelerate wound healing without scar formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WG--DTLNCWML-----SAFSR------YARCLAEG---HDGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
‡a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carries a phenol hydroxylase protein. This sequence represents phenol hydroxylase protein encoded by the sequence represented AAA11713 which is described in the method of the invention.
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                                                                                                                                                                                                    Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                          Comamonas testosterroni R5 phenol hydroxylase protein #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                Phenol hydroxylase; microbe; phenol decomposition
                                                                                                                                                                                                     DB 19;
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                                                                                                                                                                                                  Query Match 100.0%; Score 192; DB 198 Esst Local Similarity 100.0%; Pred. No. 2e-18; Matches 33; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                          1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2a; Page 15-16; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                         AAW90949 standard; Protein; 584 AA
                                          Claim 4; Fig 2B; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.4%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0243249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0243249
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Comamonas testosterroni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-264445/23
                                                                                                                                                        per kg body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 AA;
                                                                                                                                                                               33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .N-PSDB; AAA11713
                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2000069968-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2000
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                AAW90949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                AAW90949
                                                                                                                                                                                                                                                                                                    RESULT
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Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang SC;
                                                                                                                                                                                                                                              leukaemia;
                                                                                                                                                                                                               Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spiro PA, Banville SC, Shah P, Chalup MS, Chansa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Flores V, Fong WT, Greenawalt LB, Hillman JL, Vaberry AM, Rosen BH, Russo FD, Stockdreher TK, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen Wodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                             Human diagnostic and therapeutic polypeptide (DITHP) #111.
AAU19525 standard; Protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2001; 2001WO-US06059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0205324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panzer SR, Sp.r.
Chen A, D'Sa SA, Ams.r.
Dufour GE, Flores V, Foor
'4u TF, Roseberry AM, RC
'7. Yap PE, Yu J
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dulous
Liu TF, Rosencas,
Wright RJ, Yap PE,
                                                                                                                                                                                                                                                                                                    respiratory disorder
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N-PSDB; AAS31096.
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English.

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Gaps

14;

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The invention relates to identifying target proteins (ABB90790-ABB940)16) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are useful as herbicides.
comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus protein bound arrestin protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a specifically claimed protein sequence from the present invention. The present invention describes Hepatitis B virus (HBV) protein bound arrestin. Also described is a method for the preparation of the novel protein and polynucleotide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 326;
                                                                                                                                                                                                                                                                                                                Length 694;
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    255 GTVWWG.ALMMIAYFVAAHAAGACWYLLGVQRSAKCLKE 293
                                                                                                                                                                                                                                                                                                                                                                                56
                                                                    Claim 5; SEQ ID NO 3024; 261pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                ----CWMLSAFSRYARCLAE
                                                                                                                                                                                                                                                                                                              Score 55; DB 23;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53.5; DB
Pred. No. 47;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 FWGDTLNCWMLSAFSRYARCLAEGHDGPTQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus; HBV; arrestin; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus protein bound arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB23939 standard; Protein; 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 13; 16pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                              28.6%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98CN-0125693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98CN-0125693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.9
Best Local Similarity 40.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 35.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                2 GT-FWGDTLN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-544292/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UYFU-) UNIV FULAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 AA;
                                                                                                                                                                                                                                                                             694 NA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA99087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1998;
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                                     organisms
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB23939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu Γ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
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                                                       The Invention relates to polymucleotides (1) encouing alagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) and be used to treat diseases, for example, cell proliferative disorder, crown's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leuwaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPS, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and the obstruction of the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative complementary sequences may also be used as DNA probes in an diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used expression and activity and activity of the anti-DITHP antibodies and antagonists may also be used to accompanies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ARCLAEGH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                             antibodies may also be used as diagnostic agents for detecting the presence of DITHPS in samples (e.g. by enzyme linked immunosorbant asasy (ELISA)), AAO1941-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; D
Pred. No. 17;
5; Mismatches
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                                                    relates to polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FWGDTLNCW------MLSAFSRY----
              Claim 27; Page 464; 522pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB93813 standard; Protein; 694 AA
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22.6%;
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Best Local Similarity 22.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
DG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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us-09-989-481-4.rag

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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dr primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
colligonucleotide comprises at least 15 nucleotides, or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 1'-end sequence, where the
complementary strand of a sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs: The primers are also useful for the
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs: The primers allow obtaining of the full-length
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs: The primers allow obtaining of the full-length
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs: The primers allow obtaining of the full-length
connection and/or diagnosis of the shoot and sequences.

AMBISAS TEPPESSENT NAME AS REPRESSENT TEPPESSENT NAME AS AND AS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length bonAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Ya
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 15935; 2537pp + CD ROM; English.
Human protein sequence SEQ ID NO:15935
                                                                                                                                                           AAB94802 standard; Protein; 384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2000; 2000JP-0183767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37-FEB-2001
                                                                                                                                                                                                                  AAB94802;
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                                                                                                         RESULT 6
                                                                                                                                  AAB94802
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Yamamoto J;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The continuity are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving act of supplement. (II) and itssue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capping to generate disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and can main action at an invente or her trains on the printed or condition and sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.6%; Score 53; DB 22; Length 794; 40.7%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.4e+02;
3; Mismatches 13;
                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 56026; 103pp; English
FWGDTLNCWMLSAFSRYARCLAEGHDGPTQ
                                                                                                                                                                                                                                               Novel human diagnostic protein #25658.
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                                                                                                                                   ABG25667 standard; Protein; 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.69
Best Local Similarity 40.79
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS89854
                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  11-0CT-2001
                                                                                                                                                                      ABG25667;
                                                                                                RESULT 7
                                                                                                                   ABG25667
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7 DTLNCWMLSAFSRYARCLAEGHDGPTQ 33

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Gaps

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27.9%; Score 53.5; DB 22; Length 384; 40.0%; Pred. No. 56; Live 6; Mismatches 11; Indels 1;

Conservative

Local Similarity

Query Match Matches

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26
  Homo sapiens.
                                                                                                   31-JAN-2000;
                                                                                                                04-FEB-2000;
07-JUN-2000;
                                                                                                                                       14-SEP-2000;
17-NOV-2000;
                                                                                                                                                               01-DEC-2000;
                                                  02-AUG-2001
                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ovarian antigen; ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; hyperproliferative disorder; hair loss; urinary system disorder; cardiovascular disorder; arrhythmia; respiratory disorder; musculoskeletal system disorder; neutrinty disorder; neutrological disorder; endocrine disorder; gastrointestinal disorder; neutological disorder; endocratic disorder; gall bladder disorder; large intestine disorder; developmental disorder; large intestine disorder; developmental disorder; inherited disorder; wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The gene product may be isolated from a transformed expression sytem, and may be enhanced with stability in heat, alkalai, acid and organic solvent by position-specific modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                            Gene for coding protein with lipase activity – is prepd. from messenger ribonucleic acid of geo-trichum candidum ATCC 34614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 52; DB 12;
40.0%; Pred. No. 1.3e+02;
tive 1; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LGTFWGDTL----NCWMLSAFSRYARCLAEGHD 29
 DALNLFPLQINPHFTNALAEGHKGETR 765
                                                            AAR10330 standard; Protein; 563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                      Gene product with lipase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG60253 standard; Protein; 56
                                                                                                                                                                                                                                                                89JP-0074721
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                                                                                                                                                                                                                                                                                                                  (KURK ) KURITA WATER IND KK.
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                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ovarian antigen #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 40.0 ies 14; Conservative
                                                                                                                                                                                       Geotrichum candidum.
                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-027567/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 AA;
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ10313.
                                                                                                                                                                                                               JP02299588-A.
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                                                                                                                                                                                                                                                                                       27-MAR-1989;
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                                                                                                              05-APR-1991
                                                                                                                                                                                                                                       11-DEC-1990
                                                                                                                                                              ATCC 34614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
739
                                                                                    AAR10330;
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Matches
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                                                AAR10330
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                                    RESULT
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The invention relates to isolated ovarian related polypeptide (ovarian antigen) comprising a sequence at least 90% identical to a sequence selected from a polypeptide fragment, domain, epitope or full length protein of a sequence (S1) appearing as ABG60239-ABG60296 having biological activity, or a variant, allelic variant or species homologue of S1. Also included are the cDNA clones encoding the proteins of S1. S1. antibody and the cDNA clones encoding the proteins of S1. S1. antibody and the CDNA are useful for diagnosing, preventing, treating or ameliorating a medical condition in mammalian subject especially diseases and/or disorders (such as ovarian Kukenberg tumour and cancer), infectious diseases (e.g., mastitis, oophoritis), and/or breast such as neoplastic disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), comperpoliferative disorders, unimary system disorders (dlomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders (alsorders of the large intestine, developmental and inherited epithelial cell proliferation. They are also useful to prevent skin caping, for preventing hair loss, to madulate mammalian enemants of primary tissues, to modulate mammalian enemants. Or primary contraction and mammalian enemants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammallan metabolism, to change a mammal's mental or physical state, and as food additive or preservative. The present sequence represents an ovarian antigen, SI protein of the invention. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                        2000US-0232398.
2000US-0249300.
2000US-0250160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20000S-0251868.
20000S-0251990.
                                                                                                                                                                       17-JAN-2001; 2001WO-US01360
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2000US-0209467
                                                                                                                                                                                                                                                               200)0US-0179065
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WO200155329-A2.
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08-DEC-2000;
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26.6%; Score 51; DB 22; Length 56;

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1-SEP-2000;
1-SEP-2000;
                                                                                                                                               29-SEP-2(
                                                                                                   Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
       Gaps
       ñ
                                                                                        Human reproductive system related antigen SEQ ID NO: 3081.
       Indels
       5.
 Pred. No. 15;
1; Mismatches
                                                       AAM94423 standard; Protein; 56 AA
                       25 LNCWHLSCFNHALRLSCLA 43
                 9 LNCWMLSAFSRYAR--CLA 25
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                    17-JAN-2001; 2001WO-US01339
                                                                            21-NOV-2001 (first entry)
                                                                                                                              WO200155320-A2.
                                                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                  14-AUG-2000;
                                                                                                                                         02-AUG-2001.
                                                                  AAM94423;
                                            RESULT 10
                                                   AAM94423
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2000US-198123P.
2000US-205515P.
2000US-209467P.
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                                                                                                                                                 2000US-214886P
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20000S-220964P
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                                                                                 02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                               20-JUL-2001;
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26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-JUL-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                               8-AUG-2000
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           18-APR-2002
                                                                           24-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer; hyperproliferative disorder; adult acute lymphocytic leukaemia; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; Chediak Higashi's syndrome; neonatal neutropenia autoimmune disorder; Chediak Higashi's syndrome; neonatal neutropenia; septic shock; multiple sclerosis; central nervous system disorder; neurological disorder; atherosclerosis; blood related disorder; cardiovascular disorder; atherosclerosis; blood related disorder; respiratory disorder; uninary system disorder; musculoskeateal disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 3081; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ovarian related polypeptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG61724 standard; Protein; 56 AA
                                                                                                                                                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LNCWMLSAFSRYAR -- CLA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 LNCWHLSCFNHALRLSCLA 43
                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                            2000US-0251988.
2000US-0256719.
                                                                                                                           2000US-0251856
2000US-0251868
                                                                                                                                                 000US-0251869
                                                                                                                                                         00000S-0251989
                                                                                                                                                                                         05-JAN-2001; 2001US-0259678
                    000US-0249265
                                                              2000US-0250160
                                2000US-0249297
                                                                                                                                                                               0000S-0254097
                                                                        10000S-0250391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                       WPI; 2001-465570/50.
N-PSDB; AAL00393.
                                                                                                                                                                                                                                                                                                                                                                                                 56 AA;
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                                                            01-DEC-2000)
01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
08-DEC-2000)
08-DEC-2000)
                                        17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
                               17-NOV-2000;
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                                                                                                                                                                                                                                   Rosen CA,
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Gaps
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                                                                                                                                                                                                                                                                                            Score 51; DB 23; Length 56;
Pred. No. 15;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 6-phospho-strand-glucosidase #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parse"
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/note="GG dipeptide pa.
14.20
/note="Strand B"
/note="Strand B"
/note="Pa-
                                                                                                                                                                                                                                                                                                                                                                                                   AAE23630 standard; Protein; 466 AA
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/note= "Strand A"
50..54
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                                                                                                                                                                                                                                                                                                                                           25 LNCWHLSCFNHALRLSCLA 43
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2001US-0764874.
2001US-0764882.
2001US-0764888.
2001US-0764891.
2001US-0764892.
2001US-0764896.
                                                                                                                                                                                                                                                                                            Query Match 26.6%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                    2001US-0764902
2001US-0764905
                                                                                                                     2001WO-US01320
                                                                                        2001WO-US01239
                                                                                                  2001WO-US01307
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/note= '
62..63
/note= "
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                                                                                                                                                                                                                                            (ROSE/) ROSEN C A.
(RUBI/) RUBIN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                             7-JAN-2001;
7-JAN-2001;
                                                7-JAN-2001;
                                                          17-JAN-2001;
17-JAN-2001;
                                                                                                          17-JAN-2001;
17-JAN-2001;
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"GG dipeptide parse"

Region 275.280  Region /note="Strand Y"  Region 286.293  Region 318.320  Region /note="Strand Y"  Region /note="Strand F"  Region /note="Helix Y"  Region /note="Helix Y"  Region /note="Helix Y"  Region /note="Strand E"  Region /note="Strand E"  Region /note="Strand F"  Region /note="Strand F"
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Methods for excluding or detecting homology between protein families, useful e.g. for identifying in vitro properties of proteins important for physiological activity -

The invention relates to a method for excluding homology between two protein families. The method involves constructing models for secondary structural elements for each family; allyaning secondary structural elements for one family with the secondary structural elements for one family with the secondary structural elements fine the other family structural elements fine the sequence motifs; determining whether secondary structural elements in the other family; so as to determine if the families are related by common ancestry or not. The method is used to confirm/deny the hypothesis that proteins are homologous and related methods are chypothesis that proteins are homologous and related methods are used to identify in viro properties of proteins that are important for physiological activity and to generate genome-sized databases.

The present sequence is Escherichia coli 6-phospho-strand-glucosidase (EC 3.2.1.86). This sequence is used in the exemplification of the

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ftp.wipo.int/pub/published_pct_sequences
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20-JUN-2000;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                      AAM78524;
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Zhao QA,
                                           Sequence
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                                                                                                                                                                                                                                                                        RESULT 14
SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are pseudomonas aeruginosa and Enterococcus facefals. The premumniae, Pseudomonas aeruginosa and Enterococcus facefals. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expresse proteins.

The proteins can be used to screen compounds in rational drug discovery of programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of termat directly from WIPO at
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                                                                               Length 466;
                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                               DB 23;
                                                                               Score 51; DB 23;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli cellular proliferation protein #258.
                                                                                                                                                                                             Example 3; Seq ID No 10270; 511pp; English.
                                                                                                                          3; Mismatches
                                                                                                                                                                   1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30
                                                                                                                                                                                                                                                                                                               AAU34677 standard; Protein; 474 AA.
                                                                               26.68;
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2000US-207727P.
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Xu HH;
                                                                                                                          13; Conservative
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N-PSDB; AAS52536.
                                                                                                       Best Local Similarity
                                           466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
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Yamamoto RT,
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  invention.
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                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Asundl V, Zhou P, Xu C, Cao Y, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Wejhrman T, Goodrich R;
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                                                      Length 474;
                                                                                                                       Indels
                                                      Score 51; DB 22;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                    1 LGTFWGDTLNCWMLSAFSRYARCLAEGHDG 30
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                                                                                                                                                                                                                                                                                                                                                                                                     AAM78524 standard; Protein; 1207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein SEQ ID NO 1186.
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2000US-0598075.
2000US-0620325.
2000US-0654936.
                                                         26.6%;
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20-OCT-2000; 2000US-0693325
30-NOV-2000; 2000US-0728422
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                                                         Query Match 26.6
Best Local Similarity 43.3
Matches 13; Conservative
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N-PSDB; AAK51657.
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Wang D,
Yang Y, W
474 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet-derived growth factor; PpGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF; transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator; dermal ulcer; wound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                                                                                                         Gaps
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                                                                    Length 1207;
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                                                                  Score 51; DB 22; Length 12
Pred. No. 4.1e+02;
2; Mismatches 5; Indels
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841 SMYARCISEGEDATCQ 856
                                                                    26.6%;
56.2%;
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les 9; Conserv
                  1207 AA
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(PFIZ ) PFIZER INC.
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Matches
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1207 AA

Sequence

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Length 1207;
Score 51; DB 22; Length 12
Pred. No. 4.1e+02;
!; Mismatches 5; Indels
26.6%;
56.2%;
Query Match
Best Local Similarity 56.2
Matches 9; Conservative
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33 18 SRYARCLAEGHDGPTQ

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Search completed: May 29, 2003, 15:43:06 Job time: 71 secs

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